

SEQUENCE LISTING



#5/a
FEB 25 1999

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Lal, Preeti
Tang, Y. Tom
Yue, Henry
Corley, Neil C.

(ii) TITLE OF THE INVENTION: KINESIN LIGHT CHAIN HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0484 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01
(B) CLONE: 2479739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Gly	Leu	Val	Leu	Gly	Gln	Arg	Asp	Glu	Pro	Ala	Gly	His	Arg
1							5			10				15	
Leu	Ser	Gln	Glu	Glu	Ile	Leu	Gly	Ser	Thr	Arg	Leu	Val	Ser	Gln	Gly
								20		25			30		
Leu	Glu	Ala	Leu	Arg	Ser	Glu	His	Gln	Ala	Val	Leu	Gln	Ser	Leu	Ser
							35		40			45			
Gln	Thr	Ile	Glu	Cys	Leu	Gln	Gln	Gly	Gly	His	Glu	Glu	Gly	Leu	Val
							50		55			60			

His Glu Lys Ala Arg Gln Leu Arg Arg Ser Met Glu Asn Ile Glu Leu
 65 70 75 80
 Gly Leu Ser Glu Ala Gln Val Met Leu Ala Leu Ala Ser His Leu Ser
 85 90 95
 Thr Val Glu Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu
 100 105 110
 Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu Leu Ala Gly Thr Gln Gln
 115 120 125
 Arg Leu Gln Arg Ser Glu Gln Ala Val Ala Gln Leu Glu Glu Glu Lys
 130 135 140
 Lys His Leu Glu Phe Leu Gly Gln Leu Arg Gln Tyr Asp Glu Asp Gly
 145 150 155 160
 His Thr Ser Glu Glu Lys Glu Gly Asp Ala Thr Lys Asp Ser Leu Asp
 165 170 175
 Asp Leu Phe Pro Asn Glu Glu Glu Asp Pro Ser Asn Gly Leu Ser
 180 185 190
 Arg Gly Gln Gly Ala Thr Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro
 195 200 205
 Ala Arg Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ala Gln
 210 215 220
 Gly Arg Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp
 225 230 235 240
 Leu Glu Arg Thr Ser Gly Arg Gly His Pro Asp Val Ala Thr Met Leu
 245 250 255
 Asn Ile Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Glu Ala
 260 265 270
 Ala His Leu Leu Asn Asp Ala Leu Ser Ile Arg Glu Ser Thr Leu Gly
 275 280 285
 Pro Asp His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu
 290 295 300
 Tyr Gly Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Gln Arg
 305 310 315 320
 Ala Leu Glu Ile Arg Glu Lys Val Leu Gly Thr Asn His Pro Asp Val
 325 330 335
 Ala Lys Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys
 340 345 350
 Tyr Glu Ala Val Glu Arg Tyr Tyr Gln Arg Ala Leu Ala Ile Tyr Glu
 355 360 365
 Gly Gln Leu Gly Pro Asp Asn Pro Asn Val Ala Arg Thr Lys Asn Asn
 370 375 380
 Leu Ala Ser Cys Tyr Leu Lys Gln Gly Lys Tyr Ala Glu Ala Glu Thr
 385 390 395 400
 Leu Tyr Lys Glu Ile Leu Thr Arg Ala His Val Gln Glu Phe Gly Ser
 405 410 415
 Val Asp Asp Asp His Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu
 420 425 430
 Glu Met Ser Lys Ser Arg His His Glu Gly Gly Thr Pro Tyr Ala Glu
 435 440 445
 Tyr Gly Trp Tyr Lys Ala Cys Lys Val Ser Ser Pro Thr Val Asn
 450 455 460
 Thr Thr Leu Arg Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Leu
 465 470 475 480
 Glu Ala Ala Glu Thr Leu Glu Glu Cys Ala Leu Arg Ser Arg Arg Gln
 485 490 495
 Gly Thr Asp Pro Ile Ser Gln Thr Lys Val Ala Glu Leu Leu Gly Glu
 500 505 510
 Ser Asp Gly Arg Arg Thr Ser Gln Glu Gly Pro Gly Asp Ser Val Lys
 515 520 525
 Phe Glu Gly Gly Glu Asp Ala Ser Val Ala Val Glu Trp Ser Gly Asp
 530 535 540
 Gly Ser Gly Thr Leu Gln Arg Ser Gly Ser Leu Gly Lys Ile Arg Asp
 545 550 555 560
 Val Leu Arg Arg Ser Ser Glu Leu Leu Val Arg Lys Leu Gln Gly Thr
 565 570 575
 Glu Pro Arg Pro Ser Ser Ser Asn Met Lys Arg Ala Ala Ser Leu Asn
 580 585 590
 Tyr Leu Asn Gln Pro Ser Ala Ala Pro Leu Gln Val Ser Arg Gly Leu

595	600	605
Ser Ala Ser Thr Met Asp Leu Ser Ser Ser		
610	615	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
- (B) CLONE: 2479739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAAGTGGT	GAAAGAAGGG	GTGGGAACGC	TGGACTTCTG	GACTTTGGC	AGGGCAGATC	60
CTCTGACTCT	CTGGCTGCAG	AACAGTTCT	TCCGTGCTCT	GGCCTGAGTG	CCCACAGGCC	120
AGGGGCCTCT	GCTCTGTACA	CAGACCGGGC	AAGGTCCCCC	AGGCCAGGAT	GTCAGGCCTG	180
GTGTTGGGGC	AGCGGGATGA	GCCTGCAGGC	CACCAGCTCA	GCCAAGAGGA	GATCCTGGGG	240
AGCACACGGC	TGGTCAGCCA	AGGGCTAGAG	GCCCTACGCA	GTGAACACCA	GGCCGTGCTG	300
CAAAGCCTGT	CCCAAGACCAT	TGAGTGTCTG	CAGCAGGGAG	GCCATGAGGA	AGGGCTGGTG	360
CATGAGAAGG	CCCGGCAGCT	TCGCCGTCT	ATGGAAAACA	TTGAGCTCGG	GCTGAGTGAG	420
GCCCAGGTGA	TGCTGGCTCT	AGCCAGCCAC	CTGAGCACAG	TGGAGTCGGA	GAAACAGAAAG	480
CTGCGGGCTC	AGGTGCGGGC	GCTATGCCAG	GAGAACAGGT	GGCTGCCGGG	TGAGCTGGCT	540
GGCACCCAGC	AGCGGGCTACA	GCGCAGTGAA	CAGGCTGTGG	CTCAGCTGGA	GGAGGAAAAG	600
AAGCACCTGG	AGTCTCTGGG	GCAGCTCGGG	CAGTATGATG	AGGATGGACA	TACCTCGGAG	660
GAGAAAGAAG	GCGATGCCAC	CAAGGATTCC	CTGGATGACC	TCTTCTCTAA	TGAGGAGGAA	720
GAGGACCCCA	GCAATGGCTT	GTCCCCGTGGT	CAAGGTGCTA	CAGCAGCTCA	GCAGGGTGGA	780
TATGAGATCC	CAGCAAGGTT	GC GGACGTTG	CACAACCTGG	TGATCCAGTA	CGCAGCCCCAA	840
GGTCGCTATG	AGGTGGCCGT	GCCACTCTGT	AAGCAGGCAC	TAGAGGACCT	GGAGCGCACA	900
TCAGGCCGTG	GCCACCCCTGA	TGTCGCCACC	ATGCTCAACA	TCCTTGCTTT	GGTGTATCGT	960
GACCAGAATA	AGTATAAGGA	AGCTGCCAC	CTGCTGAATG	ATGCCCTTAG	CATCCGGGAG	1020
AGCACCTTGG	GACCTGACCA	TCCTGCTGTG	GCTGCCACAC	TCAACAATT	GGCTGTGCTC	1080
TATGGCAAA	GGGGCAAGTA	CAAGGAGGCA	GAGCCTCTGT	GCCAGCGGGC	ACTGGAGATT	1140
CGAGAAAAGG	TCCTGGGCAC	GAATCATCCA	GATGTGGCAA	AACAGCTGAA	CAACCTGGCC	1200
CTCTTGTGCC	AAAACCAGGG	CAAGTATGAG	GC CGTGGAAAC	GCTACTACCA	GCGAGCACTG	1260
GCCATCTACG	AGGGGCAGCT	GGGGCCGGAC	AACCCTAATG	TAGCCCGGAC	CAAGAACAAAC	1320
CTGGCTTCTC	GT TACCTGAA	ACAGGGCAA	TATGCTGAGG	CTGAGACACT	ATACAAAGAG	1380
ATCCTGACCC	GTGCCCATGT	ACAGGAGTTT	GGGTCTGTGG	ATGATGACCA	CAAGCCCCATC	1440
TGGATGCATG	CAGAGGAGCG	GGAGGAAATG	AGCAAAAGCC	GGCACCATGA	GGGTGGGACA	1500
CCCTATGCTG	AGTATGGAGG	CTGGTACAAG	GCTGCAAAG	TGAGCAGCCC	CACAGTGAAC	1560
ACTACTCTGA	GAAACCTGGG	AGCTCTGTAT	AGGCGCCAGG	GAAAGCTGGA	GGCTGCTGAG	1620
ACCCCTGGAGG	AATGTGCCCT	CGGGTCCCAGG	AGACAGGGCA	CTGACCTAT	CAGCCAGACG	1680
AAAGGTGGCAG	AGCTGCTTGG	GGAGAGTGAT	GGTAGAAGGA	CCTCCAGGA	GGGCCCTGGA	1740
GACAGTGTGA	AATCGAGGG	TGGTGAAGAT	GCTTCTGTGG	CTGTGGAGTG	GTCCGGGGAT	1800
GGCAGTGGGA	CCCTGCAGAG	GAGTGGCTCT	CTTGGCAAGA	TCCGGGATGT	GCTCCGCAGA	1860
AGCAGTGAAC	TCTGGTGAG	GAAGCTCCAG	GGGACTGAGC	CTCGGCCCTC	CAGCAGCAAC	1920
ATGAAGCGAG	CAGCCTCCTT	GAACTATCTG	AACCAACCTA	GTGCAGCACC	CCTCCAGGTC	1980
TCCCCGGGCC	TCAGTGCCAG	CACCATGGAC	CTCTCTTCAA	GCAGCTGACA	TTCAACCCGG	2040
CCCCCAGGTC	TGCTGGGTGG	CCCCACCCCC	ACAGCCCTCA	CAGCATTCCC	CATTGCTCT	2100
GGCTCTTCCC	CACCCCTAGG	TGGGACAGTG	AAGGGGAGCA	GT TAAACCGA	AAGATTGCTG	2160
CTGCCCTTAG	GGTCTCAGCT	CCCTCTCAG	GAATCCCTCT	TAGGAAGGAC	CCTCAGGACA	2220
CCCTCTCTGC	ACCCTGTGGT	CCTCTAGAGT	AGCTAGCTCT	GAGGCCCAA	GGTGGGTACA	2280
AAGCAGGTAT	GGCCCTCAGA	GATGCAGCCT	GCTGCTGGCT	TTTCAGTCAG	AGGGTTGGGG	2340
GCTGGCCAGC	CAAGCTGCCT	TGCCCTGGCC	GCTCTTACTC	CCTCCCTCTG	CTGTCTCACT	2400
TCAGGTCCAT	GTATTTCACT	TTTCTTAAAT	AAAAGAATCA	GTNCTNTNT	NNG	2453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 307085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
 1 5 10 15
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 20 25 30
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
 35 40 45
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
 50 55 60
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
 65 70 75 80
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
 85 90 95
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
 100 105 110
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
 115 120 125
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Lys Lys His Leu
 130 135 140
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
 145 150 155 160
 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
 165 170 175
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
 180 185 190
 Ser Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
 195 200 205
 Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
 210 215 220
 Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
 225 230 235 240
 Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile
 245 250 255
 Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
 260 265 270
 Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
 275 280 285
 His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
 290 295 300
 Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
 305 310 315 320
 Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
 325 330 335
 Gln Leu Asn Asn Leu Ala Leu Cys Gln Asn Gln Gly Lys Tyr Glu
 340 345 350
 Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
 355 360 365
Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
 370 375 380
 Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
 385 390 395 400
 Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp
 405 410 415
 Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys
 420 425 430
 Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp
 435 440 445
 Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Leu Lys
 450 455 460
 Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu
 465 470 475 480
 Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn

	485		490		495										
Val	His	Lys	Gln	Arg	Val	Ala	Glu	Val	Leu	Asn	Asp	Pro	Glu	Asn	Met
			500				505						510		
Glu	Lys	Arg	Arg	Ser	Arg	Glu	Ser	Leu	Asn	Val	Asp	Val	Val	Lys	Tyr
			515				520						525		
Glu	Ser	Gly	Pro	Asp	Gly	Gly	Glu	Glu	Val	Ser	Met	Ser	Val	Glu	Trp
			530				535				540				
Asn	Gly	Gly	Val	Ser	Gly	Arg	Ala	Ser	Phe	Cys	Gly	Lys	Arg	Gln	Gln
			545				550			555				560	
Gln	Gln	Trp	Pro	Gly	Arg	Arg	His	Arg							
			565												